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LISTING OF THE CLAIMS:

1. (Previously presented) A method of identifying a compound that binds to a nuclear receptor coactivator binding site, said method comprising:

modeling a test compound that fits spatially into the nuclear receptor coactivator binding site using an atomic structural model of the nuclear receptor coactivator binding site or portion thereof; and

screening said test compound in an assay that measures binding of the test compound to the nuclear receptor coactivator binding site, thereby identifying a test compound that binds to the nuclear receptor coactivator binding site.

2. (Previously presented) The method of claim 1, wherein said atomic structural model is a model of human thyroid beta receptor and comprises atomic coordinates of amino acid residues selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454, as shown in Figure 19.

3. (Previously presented) The method of claim 1, wherein said atomic structural model is a model of human thyroid beta receptor and comprises atomic coordinates of amino acid residues selected from the group consisting of Val284, Lys288, Ile302, Lys306, Leu454 and Glu457, as shown in Figure 19.

4. (Previously presented) The method of claim 1, wherein said atomic structural model is a model of human thyroid beta receptor and comprises atomic coordinates of amino acid residues selected from the group consisting of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, Lys288, helix 4 residue Phe293, helix 5 residues Gln30l, Ile302, Leu305, Lys306, helix 6 residue Cys309, helix 12 residues Pro453, Leu454, Glu457, Val458, and Phe459, as shown in Figure 19.

5. (Previously presented) The method of claim 1, wherein said nuclear receptor coactivator binding site is a coactivator binding site of human thyroid beta receptor and comprises amino acid residues selected from the group consisting of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457, Val458 and Phe459, as shown in Figure 19.